

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PARANHOS-BACCALA, Glauzia  
LESENECHAL, Mylene  
JOLIVET, Michel
- (ii) TITLE OF INVENTION: NEW TRYPANOSOMA CRUZI ANTIGEN, AND  
GENE ENCODING THE LATTER; THEIR APPLICATION TO THE  
DETECTION OF CHAGAS DISEASE

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Oliff & Berridge  
(B) STREET: 700 South Washington Street, Suite 300  
(C) CITY: Alexandria  
(D) STATE: Virginia  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22314

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/480,917  
(B) FILING DATE: 07-JUN-1995  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Berridge, William P.  
(B) REGISTRATION NUMBER: 30,024  
(C) REFERENCE/DOCKET NUMBER: WPB 36400

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 703-836-6400  
(B) TELEFAX: 703-836-2787

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3402 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACGCTATTA TTAGAACAGT TTCTGTACTA TATTGTCATT TGGGGAGGGG GGAAAGGGGG	60
GAAGTACTTG CCGTTTGTG TGGGTGACGA GACAACACAC ATCGAGCGGG AAGAAAAAAA	120
AAAAGGAAAT AAATTAAATT AAATTATTTG TTCTTTGAAT AGGCAGAGAA GAAGAAGAAG	180

AAAAGGTGCG	GGGGAGGGAG	GAGAAAGCGA	CACACACACA	AAAAAAAAAA	AAGGAATTGC	240
GGAAATAACA	ACGCAAGGCG	CGGACATGAC	CGTACGGTG	GATTGTTCA	ATCATGCGAA	300
GCCGAGCAAC	AATGAGGGCC	GCGTGTGGTC	TGTGGACGCC	GCGACATTAA	ACGAGGTGCC	360
TGAGGCGCAG	CGTGTGCTGG	CGGATTGCA	GTTTATCTT	GCCTACACCA	TGAAGCGGCG	420
TCACGTGCTG	CGTGTGGTGA	AGCGCTCGAA	CCTTTGAAG	GGCACCGTGC	GGGCACACTC	480
AAAGCCCATT	CATGCGGTGA	AGTTTGTGAA	TTACCGCAGT	AACGTCGCAG	CATCGGCTGG	540
GAAGGGGAG	TTCTCGTGT	GGGTTGTGAC	GGATGAAACG	GAGGCGAGCA	ACGGCAAGCC	600
GGATCTCGCA	GCCCCCCTCA	CAGTGAAGGT	GTACTTTAAG	CTTCAGGATC	CTGTCACAAT	660
TCCATGCTTT	TCTTCTTTA	TCAACGCCGA	GAGTCAGCGG	CCTGATCTGC	TTGTCCTTTA	720
CGAAACGCAG	GCGGCAATT	TTGACAGCTC	CTCCCTCATT	GAGCGTTTG	ACGTGGAATC	780
ACTGGAGGCA	ACACTACAGC	GGAATTGCAC	AACCCCTGCGA	ACCCCTGACTC	AACCGGTTAG	840
TGAGAACAGT	TTATGCTCCG	TTGGCTCTGG	CGGATGGTTC	ACCTTTACCA	CGGAACCAAAC	900
AATGGTAGCG	GCATGCACAT	TACGAAACCG	CAGCACTCCA	TCATGGCGGT	GTTGCGAGGG	960
TGAGCCAGTG	AAGGCATTGC	ATCTCCTTGA	CGCAACCGTT	GAGGAAAATG	TCAGTGTCT	1020
CGTGGCCGCA	TCTACAAAAG	GGGTGTACCA	ATGGCTCCTT	ACGGGTGTAG	CAGAACCAAA	1080
CTTGTGCGC	AAGTTTGTCA	TTGATGGATC	TATTGTCGCG	ATGGAAAGCT	CACGAGAAC	1140
GTGGCCGTG	TTTGACGACA	GGAAGCAGCT	GGCGCTGGTC	AACATGCATT	CCCCTCATAA	1200
CTTTACCTGC	ACACACTACA	TGATGCCTTG	TCAGGTACAG	CGTAACGGCT	TTTGCTTCAA	1260
TCGTACAGCC	GACGGTAGCT	GCGTCCTGGC	TGACATGTG	ATTGATTGA	CGATCTTCCA	1320
TCTCCGGTCC	TCCCGCAGGG	AAGAACAGCA	GCCAGGCCAA	AAAACATCGG	TAGTGGCGAC	1380
GGCGAAACCG	GGGTGTGTGT	CCTCGGGCAC	TGACGGCGCG	AGTAGCAGTC	ATACCAATAC	1440
GACTTCTGCC	GCTGCTGCAT	CCCCTGCATC	ACCCCTGTT	TCAGGCCAG	CCAAGGCAGC	1500
CGCGCCTCCT	GCCGCGCGC	GATCGGCTGA	CCCGCACGTG	GGGAGCAAGA	TCATTGCTAA	1560
TCTAGTGAAT	CAGCTGGGA	TTAATGTCAC	CCAAAGGAGC	GTCGTCAGCA	CTGGAGCGCC	1620
GGCCACGACG	AGGTCTACGG	CGGTGACGTC	CACGACTACC	GCCCCGCAGC	GAACAAGTCC	1680
ATACGGGCAC	AATGGCCGAC	CTGTGACGGC	TGGATTGGTG	GCAGCTAATA	GTGGTGCCAG	1740
CGCGGCCTCG	TCTCCCACAG	CCGCGCGAA	ACCAACAGGA	GAAGAAAAGG	CCTCCGCGGC	1800
ATGTGAAACG	AGCTCCGTGG	CGATAATGC	GACACGCCG	GCGCTTCACA	ACGCCTCTCT	1860
CCCGCAGGCG	CCAACGGATG	GCCTTTGGC	GGCAGCAGTA	TACCAAGTCGG	AGGGCGAGGT	1920
TCATCAGTCG	CTGGAGCGGC	TGGAGTCCGT	CATAACCAAC	ACGTCTCGGG	TTCTGAAGTT	1980
GCTCCCTGAC	ACCATTGAA	GAGACCATGA	ACAACCTCTG	AATCTGGGTT	TAGAGGCACA	2040

GATGACAGAG	CTGCAGCAGA	GCCGTCCAAC	ACCGCAAACA	CAGCCGAGAG	ACACAAGCTC	2100
CGCGAAATCA	TCCGTGTTG	AGACGTACAC	CCTTGTTC	ATTGCGGATT	CCCTCTCTCG	2160
CAACATCACG	AAGGGGGTGA	AGCGTGGTGT	GAACGAGGCC	ATTATGTTGC	ATCTCGACCA	2220
TGAGGTGCGG	CACGCCATAG	GGAACCGGCT	TCGGCAAACA	CAAAAGAAC	TCATCAAGAG	2280
CCGCCTCGAT	GAAGCGTTGA	AGGAAAGCAC	TACACAGTT	ACGGCTCAAT	TGACGCAAAC	2340
GGTGGAGAAT	CTGGTGAAAGC	GCGAGCTTGC	CGAGGTGCTT	GGTAGCATCA	ACGGCTCCCT	2400
CACTTCTCTC	GTGAAGGAAA	ATGCCTCATT	ACAGAAAGAG	TTGAATTCCA	TAATGTCTAG	2460
TGGGGTGTG	GATGAAATGC	GTCGTATGCG	GGAAGAGCTG	TGCACATTGC	GAGAGTCCGT	2520
TGCGAAGCGG	AAGGCAACAA	TGCCAGATT	TTCTCTTCAC	GCCACGAGCT	CCTTTCAAGG	2580
AAGAAGGTCT	GCGCCCGAGA	CAATTCTTGC	AACC CGTTA	TCGATGGTGC	GAGAGCAGCA	2640
ATACCGTCAG	GGACTGGAAT	ACATGTTGAT	GGCTCAGCAG	CCCTCTCTCC	TCCTGCGGTT	2700
CCTCAGCATA	CTTACAAGGG	AAAACGAAA	CGCCTACTCG	GAACTTATTG	AAAATGTAGA	2760
GACGCCGAAT	GACGTGTGGT	GTTCGGTTCT	GTTGCAA	ATAGAGGCCG	CGCGACCGA	2820
GGCTGAGAAG	GAGGTGGTTG	TTGGCGTCGC	CATTGATATT	CTCTCCGAGC	GCGATCAAAT	2880
TGCTCAGAAC	GGCGCACTCG	GCTCGAAACT	CACCACCGCC	ATGCGAGCCT	TTGAGCGACA	2940
GGCAAGGTCTG	GAGACAACGA	GCAGGTCA	CTTGCAATGC	CTGAAGAAC	TGGAAAAGCT	3000
TCTGCAATCA	TGATAATAAA	AAGAACTCAA	CGAATACAGT	TGTTGATTAT	TAAGGAAGGG	3060
AAAAGAGAGA	AAGAGAGAGA	GAGAGAGAGA	AATGTAATGG	GCCTTTAGTT	ACGGTAGAAA	3120
GAAAACGTGT	GGATAAGAAG	GAGGGGTTT	GTGTGCGACC	AGGAATTACT	GGGAAACGCT	3180
GCTACACGGC	GGAATCGACC	ATTTTATTAT	TATTATTATT	GTCTTTAGTA	TTATGTTTT	3240
TCTTGTGTGT	GTGTGTGTGT	GTGGTGTGT	GTGCGGTTAT	TTTGTATCCG	TTGCTCCCG	3300
CCCCCTGCC	CCATCACCCG	AGGAGAAAGT	AGAATAAGAC	ACATACGATT	GTTGTTTTG	3360
TTATCCTTAA	AAGGAAGAGA	GACCA	AAAAAA	AAAAAA	AA	3402

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 915 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Val Thr Val Asp Leu Phe Asn His Ala Lys Pro Ser Asn Asn  
1 5 10 15

Glu Gly Arg Val Trp Ser Val Asp Ala Ala Thr Phe Asn Glu Val Pro  
20 25 30

Glu Ala Gln Arg Val Leu Ala Asp Ser Gln Phe Tyr Leu Ala Tyr Thr  
35 40 45

Met Lys Arg Arg His Val Leu Arg Val Val Lys Arg Ser Asn Leu Leu  
50 55 60

Lys Gly Thr Val Arg Ala His Ser Lys Pro Ile His Ala Val Lys Phe  
65 70 75 80

Val Asn Tyr Arg Ser Asn Val Ala Ala Ser Ala Gly Lys Gly Glu Phe  
85 90 95

Phe Val Trp Val Val Thr Asp Glu Thr Asp Ala Ser Asn Gly Lys Pro  
100 105 110

Asp Leu Ala Ala Arg Leu Thr Val Lys Val Tyr Phe Lys Leu Gln Asp  
115 120 125

Pro Val Thr Ile Pro Cys Phe Ser Phe Phe Ile Asn Ala Glu Ser Gln  
130 135 140

Arg Pro Asp Leu Leu Val Leu Tyr Glu Thr Gln Ala Ala Ile Leu Asp  
145 150 155 160

Ser Ser Ser Leu Ile Glu Arg Phe Asp Val Glu Ser Leu Glu Ala Thr  
165 170 175

Leu Gln Arg Asn Cys Thr Thr Leu Arg Thr Leu Thr Gln Pro Val Ser  
180 185 190

Glu Asn Ser Leu Cys Ser Val Gly Ser Gly Gly Trp Phe Thr Phe Thr  
195 200 205

Thr Glu Pro Thr Met Val Ala Ala Cys Thr Leu Arg Asn Arg Ser Thr  
210 215 220

Pro Ser Trp Ala Cys Cys Glu Gly Glu Pro Val Lys Ala Leu His Leu  
225 230 235 240

Leu Asp Ala Thr Val Glu Glu Asn Val Ser Val Leu Val Ala Ala Ser  
245 250 255

Thr Lys Gly Val Tyr Gln Trp Leu Leu Thr Gly Val Ala Glu Pro Asn  
260 265 270

Leu Leu Arg Lys Phe Val Ile Asp Gly Ser Ile Val Ala Met Glu Ser  
275 280 285

Ser Arg Glu Thr Phe Ala Val Phe Asp Asp Arg Lys Gln Leu Ala Leu  
290 295 300

Val Asn Met His Ser Pro His Asn Phe Thr Cys Thr His Tyr Met Met  
305 310 315 320

Pro Cys Gln Val Gln Arg Asn Gly Phe Cys Phe Asn Arg Thr Ala Asp  
325 330 335

Gly Ser Cys Val Leu Ala Asp Met Ser Asn Arg Leu Thr Ile Phe His  
340 345 350

Leu Arg Cys Ser Arg Arg Glu Glu Gln Gln Pro Gly Gln Lys Thr Ser  
355 360 365

Val Val Ala Thr Ala Lys Pro Gly Cys Val Ser Ser Gly Thr Asp Ala  
370 375 380

Ala Ser Ser Ser His Thr Asn Thr Thr Ser Ala Ala Ala Ala Ser Pro  
385 390 395 400

Ala Ser Pro Pro Val Ser Ala Pro Ala Lys Ala Ala Ala Pro Pro Ala  
405 410 415

Ala Ala Arg Ser Ala Glu Pro His Val Gly Ser Lys Ile Ile Ala Asn  
420 425 430

Leu Val Asn Gln Leu Gly Ile Asn Val Thr Gln Arg Ser Val Val Ser  
435 440 445

Thr Gly Ala Pro Ala Thr Thr Arg Ser Thr Ala Val Thr Ser Thr Thr  
450 455 460

Thr Ala Pro Gln Arg Thr Ser Pro Tyr Gly His Asn Gly Arg Pro Val  
465 470 475 480

Thr Ala Gly Leu Val Ala Ala Asn Ser Gly Ala Ser Ala Ala Ser Ser  
485 490 495

Pro Thr Ala Ala Ala Lys Pro Thr Gly Glu Glu Lys Ala Ser Ala Ala  
500 505 510

Cys Glu Thr Ser Ser Val Ala Ile Asn Ala Thr Arg Pro Ala Leu His  
515 520 525

Asn Ala Ser Leu Pro Gln Ala Pro Thr Asp Gly Val Leu Ala Ala Ala  
530 535 540

Val Tyr Gln Ser Glu Gly Glu Val His Gln Ser Leu Glu Arg Leu Glu  
545 550 555 560

Ser Val Ile Thr Asn Thr Ser Arg Val Leu Lys Leu Leu Pro Asp Thr  
565 570 575

Ile Arg Arg Asp His Glu Gln Leu Leu Asn Leu Gly Leu Glu Ala Gln  
580 585 590

Met Thr Glu Leu Gln Gln Ser Arg Pro Thr Pro Gln Thr Gln Pro Arg  
595 600 605

Asp Thr Ser Ser Ala Lys Ser Ser Val Phe Glu Thr Tyr Thr Leu Val  
610 615 620

Leu Ile Ala Asp Ser Leu Ser Arg Asn Ile Thr Lys Gly Val Lys Arg  
625 630 635 640

Gly Val Asn Glu Ala Ile Met Leu His Leu Asp His Glu Val Arg His  
645 650 655

Ala Ile Gly Asn Arg Leu Arg Gln Thr Gln Lys Asn Ile Ile Lys Ser  
660 665 670

Arg Leu Asp Glu Ala Leu Lys Glu Ser Thr Thr Gln Phe Thr Ala Gln  
675 680 685

Leu Thr Gln Thr Val Glu Asn Leu Val Lys Arg Glu Leu Ala Glu Val  
690 695 700

Leu Gly Ser Ile Asn Gly Ser Leu Thr Ser Leu Val Lys Glu Asn Ala  
705 710 715 720

Ser Leu Lys Lys Glu Leu Asn Ser Ile Met Ser Ser Gly Val Leu Asp  
725 730 735

Glu Met Arg Arg Met Arg Glu Glu Leu Cys Thr Leu Arg Glu Ser Val  
740 745 750

Ala Lys Arg Lys Ala Thr Met Pro Asp Ser Ser Leu His Ala Thr Ser  
755 760 765

Ser Phe Gln Gly Arg Arg Ser Ala Pro Glu Thr Ile Leu Ala Thr Ala  
770 775 780

Leu Ser Met Val Arg Glu Gln Gln Tyr Arg Gln Gly Leu Glu Val Met  
785 790 795 800

Leu Met Ala Gln Gln Pro Ser Leu Leu Leu Arg Phe Leu Ser Ile Leu  
805 810 815

Thr Arg Glu Asn Glu Asn Ala Tyr Ser Glu Leu Ile Glu Asn Val Glu  
820 825 830

Thr Pro Asn Asp Val Trp Cys Ser Val Leu Leu Gln Leu Ile Glu Ala  
835 840 845

Ala Ala Thr Glu Ala Glu Lys Glu Val Val Val Gly Val Ala Ile Asp  
850 855 860

Ile Leu Ser Glu Arg Asp Gln Ile Ala Gln Asn Gly Ala Leu Gly Ser  
865 870 875 880

Lys Leu Thr Thr Ala Met Arg Ala Phe Glu Arg Gln Ala Arg Ser Glu  
885 890 895

Thr Thr Ser Arg Ser Phe Leu Gln Cys Leu Lys Asn Leu Ile Lys Leu  
900 905 910

Leu Gln Ser  
915

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phage DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phage DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACCAAG ACCAACTGGT AATG

24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGGGGCACTG ACGCGGCG

18

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "phage lambda gt10 DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTTATGAGTA TTTCTTCCAG GGT

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACGCTATTA TTAGAACAGT T

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCAGCAGCG GCAGAACT

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCCGACGG TAGCTGGCTC CT

22

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACATAATGGC CTCGTTCA CA C

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GACTCGCTGC AGATCGATT TTTTTTTT TTTT

34

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAAGAGACC ATGAACAACT T

21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACTCGCTGC AGATCGAT

18